<!--StartFragment-->GenCore version 6.2.1

OM nucleic - nucleic search, using sw model

Run on: April 29, 2008, 13:52:39 ; Search time 11061 Seconds
(without alignments)
17362.216 Million cell updates/sec

Title: US-10-532-944-7
Perfect score: 2346
Sequence: 1 gtgggcatgattcacgagca.....cgttttccatccatgtgtga 2346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9588671 seqs, 40929980300 residues

Total number of hits satisfying chosen parameters: 19177342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_in:*
13: gb_om:*
14: gb_ba:*
15: gb_htg1:*
16: gb_htg2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2346	100.0	8690	14	AJ252161	AJ252161 Alicyclob
2	2187	93.2	2187	2	DD448952	DD448952 GLUCOSIDA
3	1002	42.7	3097	14	AJ133789	AJ133789 Alicyclob
4	597.2	25.5	3854	14	AB012238	AB012238 Bacillus
5	427.4	18.2	110000	14	CP000386_21	Continuation (22 o
6	423.2	18.0	110000	14	AE017262_01	Continuation (2 of

	7	423	18.0	110000	14	CP000239_22	Continuation (23 o
	8	423	18.0	110000	14	CP000239_23	Continuation (24 o
	9	416.8	17.8	110000	2	BD455614_01	Continuation (2 of
	10	416.8	17.8	200050	14	AL591973	AL591973 Listeria
	11	416.8	17.8	349980	2	AX638811	AX638811 Sequence
	12	412	17.6	7787	2	AX416892	AX416892 Sequence
	13	409	17.4	231450	14	AL596163	AL596163 Listeria
	14	409	17.4	349980	2	AX415067	AX415067 Sequence
	15	409	17.4	349980	2	AX453571	AX453571 Sequence
	16	384.6	16.4	110000	14	CP000240_14	Continuation (15 o
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c	18	360.4	15.4	110000	14	CP000360_07	Continuation (8 of
c	19	360.4	15.4	110000	14	CP000360_08	Continuation (9 of
	20	344	14.7	110000	14	CP000411_07	Continuation (8 of
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	22	332.6	14.2	304274	14	AL935262	AL935262 Lactobaci
	23	319.8	13.6	2301	2	DD459592	DD459592 Lactobaci
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c	25	319.8	13.6	110000	14	CP000413_17	Continuation (18 o
	26	319.6	13.6	9699	14	AE012974	AE012974 Thermoana
	27	312.4	13.3	110000	14	BA000019_56	Continuation (57 o
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	32	284.4	12.1	232605	14	AE017222	AE017222 Thermus t
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	35	281.2	12.0	256992	14	AP008227	AP008227 Thermus t
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	41	268	11.4	110000	14	CP000685_32	Continuation (33 o
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	43	263.8	11.2	3484	4	AK243062	AK243062 Oryza sat
	44	262.2	11.2	2923	6	BC117888	BC117888 Mus muscu
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ALIGNMENTS

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RESULT 1
AJ252161
LOCUS       AJ252161               8690 bp    DNA     linear   BCT 15-APR-2005
DEFINITION  Alicyclobacillus acidocaldarius maltose/maltodextrine transport
            gene region (malEFGR genes, cdaA gene and glcA gene).
ACCESSION   AJ252161
VERSION     AJ252161.1  GI:6686561
KEYWORDS    alpha-glucosidase; cdaA gene; cyclomaltodextrinase; glcA gene; malE
            gene; malF gene; malG gene; MALR gene; maltose binding protein;
            maltose transport membrane protein; repressor of maltose transport
            genes.
SOURCE      Alicyclobacillus acidocaldarius
  ORGANISM  Alicyclobacillus acidocaldarius
            Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae;
            Alicyclobacillus.
REFERENCE   1
  AUTHORS   Hulsmann,A., Lurz,R., Scheffel,F. and Schneider,E.
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  TITLE     Maltose and maltodextrin transport in the thermoacidophilic
            gram-positive bacterium Alicyclobacillus acidocaldarius is mediated
            by a high-affinity transport system that includes a maltose binding
            protein tolerant to low pH
  JOURNAL   J. Bacteriol. 182 (22), 6292-6301 (2000)
   PUBMED   11053372
REFERENCE   2  (bases 1 to 8690)
  AUTHORS   Huelsmann,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-2000) Huelsmann A., Bakterienphysiologie,
            Humboldt Universitaet zu Berlin, Chausseestr. 117, 10115 Berlin,
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FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 2346;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy       1561 GTGGGCGGTTTCGCTCATCACGCTTCAGGTGAATTGCTTGCACGATGGACGCAAATGGGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7690 GTGGGCGGTTTCGCTCATCACGCTTCAGGTGAATTGCTTGCACGATGGACGCAAATGGGG 7749

Qy       1621 GCGTTCTTTCCGTTCTTTCGAAATCACAGTGCCATGGGAACGCATCGACAGGAACCTTGG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7750 GCGTTCTTTCCGTTCTTTCGAAATCACAGTGCCATGGGAACGCATCGACAGGAACCTTGG 7809

Qy       1681 GCATTCGGCCCTACGTTCGAAGCCGTCATTCGACGTGCCATCCGGCTCCGTTATCGTTTC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7810 GCATTCGGCCCTACGTTCGAAGCCGTCATTCGACGTGCCATCCGGCTCCGTTATCGTTTC 7869

Qy       1741 CTGCCTTATCTGTACACGCTCGCACGGGAAGCCCATGAGACAGGTTTACCCATGATGCGG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7870 CTGCCTTATCTGTACACGCTCGCACGGGAAGCCCATGAGACAGGTTTACCCATGATGCGG 7929

Qy       1801 CCCTTGGTGTTAGAGTATCCCGACGATCCAAACACGCACCACGTCGATGATCAGTTCCTC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7930 CCCTTGGTGTTAGAGTATCCCGACGATCCAAACACGCACCACGTCGATGATCAGTTCCTC 7989

Qy       1861 GTCGGTTCCGATCTTCTCGTGGCACCCATCCTCAAGCCGGGCATGGCCCATAGAATGGTC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7990 GTCGGTTCCGATCTTCTCGTGGCACCCATCCTCAAGCCGGGCATGGCCCATAGAATGGTC 8049

Qy       1921 TATTTGCCCGATGGAGAATGGATTGATTATGAGACGCGTGAGCGATACCAAGGGCGTCAG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8050 TATTTGCCCGATGGAGAATGGATTGATTATGAGACGCGTGAGCGATACCAAGGGCGTCAG 8109

Qy       1981 TACATCTTGACGTATGCGCCTCTCGATCGTATCCCTCTGTACGTGAGGGCAGGGAGCGCT 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8110 TACATCTTGACGTATGCGCCTCTCGATCGTATCCCTCTGTACGTGAGGGCAGGGAGCGCT 8169
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Qy       2041 ATCCCCGTGAACCTCTTGGAGCGGTCGGGCGAGACCCAGCTAGGATGGGAGATCTTCGTG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8170 ATCCCCGTGAACCTCTTGGAGCGGTCGGGCGAGACCCAGCTAGGATGGGAGATCTTCGTG 8229

Qy       2101 GACGCCAACGGTCGAGCCTCGGGTCGATGCTATGAGGACGACGGCGAGACGTTTAGCTAT 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8230 GACGCCAACGGTCGAGCCTCGGGTCGATGCTATGAGGACGACGGCGAGACGTTTAGCTAT 8289

Qy       2161 GAAGACGGCGCCTACTGTGATCGCGTGTTACAGGCCCTCGCCACCTCGGAAGGAACACTG 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8290 GAAGACGGCGCCTACTGTGATCGCGTGTTACAGGCCCTCGCCACCTCGGAAGGAACACTG 8349

Qy       2221 ATCGAATGTCATCTTGTTCAAGGATCAGGAGATGGTGGAAGTCTCGAGAGCGTTGTTCGC 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8350 ATCGAATGTCATCTTGTTCAAGGATCAGGAGATGGTGGAAGTCTCGAGAGCGTTGTTCGC 8409

Qy       2281 GTGTTCACACCAGATGACGTTCGTGAGGCTCGTGCGCAGGGCATATCGTTTTCCATCCAT 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8410 GTGTTCACACCAGATGACGTTCGTGAGGCTCGTGCGCAGGGCATATCGTTTTCCATCCAT 8469

Qy       2341 GTGTGA 2346
             ||||||
Db       8470 GTGTGA 8475
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<!--EndFragment-->